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LifeSeq® Gold
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ClustalW

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Retrieval	BLAST2	FASTA	ClustalW	GCG Assembly	Phrap	Translation

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☐ 768320CB1

☐ M95283

CLUSTAL W (1.7) Multiple Sequence Alignments

```
Sequence format is Pearson
Sequence 1: 768320CB1        1275 bp
Sequence 2: M95283           1266 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  85
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:   2        Score:20363
Alignment Score 7156
CLUSTAL-Alignment file created  [baabs4gc_.aln]
CLUSTAL W (1.7) multiple sequence alignment
```

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768320CB1       CAAGAGGTTNGGGGCTCTCTCCTTGTCAGTCGGCGCCGCGTGCGGGCTGGTGGCTCTGTG
M95283          ------------------------GGCA--CGAGGCCGCGTGCAGGCGTGTGGCTCTGTA
                                        *  **   **  ********* ***  **********,

768320CB1       GCA-------GCGGCGGCGGCAGGACTCCGGCACTATGAGCGGCTTCAGCACCGAGGAGCG
M95283          GCAATAGCGGCGGCGGCGGCGGCTGTTCCCCGGCACGATGAGCAGCTTCAGCAGCGAGGAGCG
                ***        ********** *   * ******* ****** ********* *********

768320CB1       CGCCGCGCCCTTCTCCCTGGAGTACCGAGTCTTCCTCAAAAATGAGAAAGGACAATATAT
M95283          CGCGGCGCCCTTCACCCTCGAGTACCGAGTCTTCCTCAAAAATGAAAAAGGACAATATAT
                *** ********* ****  ************************** *************

768320CB1       ATCTCCATTTCATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGGTAGTTGA
M95283          CTCTCCATTTCATGATATTCCAATTTATGCAGATAAGGAAGTGTTTCACATGGTCGTTGA
                ******************************************* ************* *****

768320CB1       AGTACCACGCTGGTCTAATGCAAAAATGGAGATTGCTACAAAGGACCCTTTAAACCCTAT
M95283          AGTGCCGCGCTGGTCGAATGCAAAAATGGAGATTGCTACAAAGGACCCTTTAAACCCAAT
                *** ** ******** **************************************** **

768320CB1       TAAACAAGATGTGAAAAAAGGAAAACTTCGCTATGTTGCGAATTTGTTCCCGTATAAAGG
M95283          TAAACAAGATGTGAAGAAAGGAAAACTCCGTTATGTTGCAAATCTGTTCCCGTATAAAGG
                *************** ********** **- ******* *** ***************

768320CB1       ATATATCTGGAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAA
M95283          ATACATCTGGAACTACGGTGCCATCCCTCAGACTTGGGAAGACCCAGGACACAATGACAA
                *** ********** ******************************** ******* **

768320CB1       ACATACTGGCTGTTGTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGT
M95283          ACACACTGGCTGTTGTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGT
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                ***  ********************************************************
768320CB1       ATGTGCAAGAGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGA
M95283          GTGTGCACGAGGGGGAGATTATCAGAGTGAAAGTTCTGGGCATTCTGGCCATGATTGATGA
                ****** ****  ** ** **   * ********** *****  **** ******** **

768320CB1       AGGGGAAACCGACTGGAAAGTCATTGCCATTAATGTGGATGATCCTGATGCAGCCAATTA
M95283          AGGGGAGACCGACTGGAAAGTCATTGCCATTAATGTGGAAGATCCTGATGCAGCCAATTA
                ****** ****************************************  ********************

768320CB1       TAATGATATCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTG
M95283          CAATGATATTAATGATGTCAAGCGGCTGAAACCTGGCTACCTGGAAGCTACTGTGGATTG
                ********  ********** * ******************  * ************** **

768320CB1       GTTTAGAAGGTATAAGGTTCCTGATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGA
M95283          GTTTAGGAGGTACAAGGTTCCAGATGGAAAACCTGAAAATGAGTTTGCTTTCAATGCAGA
                ******  ***** ******** ********** ************* ** ********

768320CB1       ATTTAAAGATAAGGACTTTGCCATTGATATTATTAAAAGCACTCATGACCATTGGAAAGC
M95283          ATTTAAAGATAAGAACTTTGCAATTGACATTATTGAAAGCACTCATGACTATTGGAGAGC
                *************  ******* ***** ***** ****** *************** ******* ***

768320CB1       ATTAGTGACTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGA
M95283          ATTAGTGACTAAGAAAACTGATGGAAAAGGAATCAGCTGCATGAACACTACAGTGTCTGA
                ****************** ************* ******** * ** ** *******

768320CB1       GAGCCCCTTCAAGTGTGATCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCACC
M95283          GAGCCCCTTCCAGTGTGATCCTGATGCTGCCAAAGCCATTGTGGATGCTTTACCGCCACC
                ********** ********************* ********************** *****

768320CB1       CTGTGAATCTGCCTGCACAGTACCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAAA
M95283          ATGTGAATCTGCCTGCACAATACCAACAGATGTGGATAAGTGGTTCCATCACCAGAAAAA
                 ****************** *********** ****************************

768320CB1       CTAATGAGATTTCTCTGGAATACAAGCTGATA-TTGCTACATCGTGTTCATCTGGATGTA
M95283          CTAAGGAAATTTCTCTGGAATACAAGCTGATAATTGCTGCATCCTACTTGTCGGAAAGTG
                ****  ** ********************** ***** **** *   *  ** *  *  **

768320CB1       TTAGAAGTAAAAGTAGTAGCTTTTCAAAGCTTTAAATTTGTAGAACTCATCTAACTAAAG
M95283          TTAGATGTGA---TAGTAGCTTTTCCAAGCTTTAAATTTATAGAACTAATCAGTC-----
                ***** ** *    *********** ************** ****** *** *** *

768320CB1       TAAATTCTGCTGTGACTAATCCAATATACTCAGAATGTTATCCATCTAA-AGCATTTTTC
M95283          -AGATTCTGCTGTCACCAATCCAGTGTATTCATACA-TTATCTATCTAAGAGCATTTATC
                 * ********** ** ****** *  ** *** *    ***** ****** ******* **

768320CB1       ATATCTCAACTAAGATAACTTTTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGA
M95283          GTGTC--AACTAAGGTAACATTTAGTTCCTGCTTAAATATCAAGGCGGTTGTAGTTTGGA
                 * **  ******* **** *****  * ************** ** ***** ******

768320CB1       AGTCACTTGTGAATAGATGTGCAAGGGGGAGCACATATTGGATGTATATGTTACCATATGT
M95283          AGTCATCTGTGACAGAGTATGCAAGATAAGTACATATTGGATGTATATGTTTGCTATGGT
                *****  *****    * ******   ** ******************** *    **

768320CB1       TAGGAAATAAAA-TTATTTTGCTG--------------------
M95283          TAGGAAATAAAAATTATTTGTTTCAAAAAAAAAAAAAAAAAAAA
                ************ ******* *
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